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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/101,132	06/30/1998	SHOJI TSUJI	760248P	9310

2292 7590 10/08/2002

BIRCH STEWART KOLASCH & BIRCH
PO BOX 747
FALLS CHURCH, VA 22040-0747

EXAMINER

GOLDBERG, JEANINE ANNE

ART UNIT	PAPER NUMBER
----------	--------------

1634

DATE MAILED: 10/08/2002

20

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary

Application No.

09/101,132

Applicant(s)

TSUJI ET AL.

Examiner

Jeanine A Goldberg

Art Unit

1634

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☒ Responsive to communication(s) filed on 12 August 2002.
- 2a) ☐ This action is FINAL. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 8-11, 14 and 16-18 is/are pending in the application.
- 4a) Of the above claim(s) _____ is/are withdrawn from consideration.
- 5) ☐ Claim(s) _____ is/are allowed.
- 6) ☒ Claim(s) 8-11, 14 and 16-18 is/are rejected.
- 7) ☐ Claim(s) _____ is/are objected to.
- 8) ☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on _____ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.
- Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
- 11) ☐ The proposed drawing correction filed on _____ is: a) ☐ approved b) ☐ disapproved by the Examiner.
- If approved, corrected drawings are required in reply to this Office action.
- 12) ☐ The oath or declaration is objected to by the Examiner.

Priority under 35 U.S.C. §§ 119 and 120

- 13) ☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some * c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
2. ☐ Certified copies of the priority documents have been received in Application No. _____.
3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).
- * See the attached detailed Office action for a list of the certified copies not received.
- 14) ☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. § 119(e) (to a provisional application).
- a) ☐ The translation of the foreign language provisional application has been received.
- 15) ☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121.

Attachment(s)

- 1) ☒ Notice of References Cited (PTO-892)
- 2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
- 3) ☐ Information Disclosure Statement(s) (PTO-1449) Paper No(s) _____.
- 4) ☐ Interview Summary (PTO-413) Paper No(s). _____.
- 5) ☐ Notice of Informal Patent Application (PTO-152)
- 6) ☐ Other: _____.

DETAILED ACTION

1. This action is in response to the papers filed August 12, 2002. Currently, claims 8-11, 14, 16-18 are pending.
2. All arguments have been thoroughly reviewed but are deemed non-persuasive for the reasons which follow.
3. Any objections and rejections not reiterated below are hereby withdrawn.

Priority

4. This application is a 371 application of PCT/JP97/03946, filed October 30, 1997 which claims priority to a Japanese document 304059/96, filed October 30, 1996.

New Matter

5. Claims 8-11, 14, 16-17 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

In the amended claims 8-9, 14, reference to "a nucleic acid comprising a nucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 2 further comprising from 15-100 additional glutamine residues" is included. The specification does not describe or discuss "a nucleic acid comprising a nucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 2 further comprising from 15-100 additional glutamine residues". Instead the specification describes "nucleic acid

Art Unit: 1634

fragment comprising a nucleic acid region encoding an amino acid sequence shown in SEQ ID NO: 2 (provide that the number of repeat units of Gln from the 166th to 188th amino acid varies between 15 and 100" (page 3, lines 5-10). SEQ ID NO: 2 of the specification contains 23 Gln repeats. This description does not support "a nucleic acid comprising a nucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 2 further comprising from 15-100 additional glutamine residues". The specification has not described a nucleic acid comprising a nucleotides sequence that encodes the amino acid sequence of SEQ ID NO: 2 further comprising 15-100 Gln repeats because there is no disclose which supports 123 Gln repeats. This rejection may be easily overcome by amending the claims in such a way to illustrate the invention of the instant specification. For example, Claim 8 may be amended to "An isolated nucleic acid encoding the amino acid of SEQ ID NO: 2." A new claim may be added "An isolated nucleic acid encoding a variant of the amino acid of SEQ ID NO: 2 wherein the variant differs from SEQ ID NO: 2 only in that between positions 166-188 of SEQ ID NO: 2 there are between 15 and 100 glutamine residues." Moreover, Claim 9 may be amended to recited "An isolated nucleic acid comprising nucleotides 49 to 3987 of SEQ ID NO: 1." A claim to the variants may be added, "An isolated nucleic acid comprising a variant of nucleotides 49 to 3987 of SEQ ID NO: 1 wherein the variant differs from SEQ ID NO: 1 only in that there are between 15 and 100 CAG or CAA repeats between nucleotides 543-612 of SEQ ID NO: 1." The concept of "a nucleic acid comprising a nucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 2 further comprising from 15-100 additional glutamine residues" does not appear to be part of the

originally filed invention. Therefore, "a nucleic acid comprising a nucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 2 further comprising from 15-100 additional glutamine residues" constitutes new matter.

In amended Claims 10-11, the claims contain the hybridization conditions of "5 x SSC, 1 x Denhardt's solution, 10% sodium dodecyl sulfate, 20mM sodium phosphate". These conditions do not appear to be taught in the specification. While, page 14, describes hybridization solution of 5 x SSC, 1 x Denhardt's solution, 10% dextran sulfate, 20mM sodium phosphate, the 10% sodium dodecyl sulfate does not appear to be described. Moreover, the nucleic acids do not appear to have been described as hybridizing to SEQ ID NO: 1. While the specification provides numerous hybridization assays, there does not appear to be a single example of hybridization with SEQ ID NO: 1. Therefore, the hybridization conditions recited in Claims 10-11 appear to be new matter. Moreover, the concept of hybridization to SEQ ID NO: 1 appears to be new matter.

In the added Claims 16-17, the claims are drawn to methods for genetic screening for SCA2 by contacting a sample with a first oligonucleotide of at least 15 nucleotides that specifically hybridizes to SEQ ID NO: 1 between 4367 and 622 and with a second oligonucleotide of at least 15 nucleotides that specifically hybridizes to the complement of SEQ ID NO: 1 between nucleotides 1 and 543. The specification does not teach a method which designs primers to the specified regions. While the specification exemplifies a single example within the genus, there is no support for any 15 or more nucleotide within 622-4367 or 1-543. The specification teaches measuring

CAG repeat units using a primer pair F-1 and R-1 (page 19). F-1 and R-1 are defined in the specification as SEQ ID NO: 7 and 8 (page 15). The specification teaches that a 630 bp of Tsp2 was sequenced and then primers F-1 and R-1 were designed such that the CAG repeat units are sandwiched between the oligonucleotides (page 15). There is no support for any 15 nucleotides that specifically hybridize between 1-543 and 622-4367. Therefore, the recitation of 15 nucleotides that specifically hybridize between 1-543 and 622-4367 constitutes new matter.

Applicant is required to cancel the new matter in the reply to this Office Action.

Claim Rejections - 35 USC § 112-Description

The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

6. Claims 10-11, 14 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Claims 10-11, 14 are broadly drawn to isolated nucleic acid comprising a 2.5 kb Tsp E1 restriction fragment of human DNA that hybridizes to the nucleotide sequence of SE QID NO: 1 under specified hybridization conditions. The claims are further drawn to a nucleic acid comprising a 630 Sma I-Apa I restriction fragment of human DNA that

hybridizes to the nucleotide sequence of SEQ ID NO: 1 under specified hybridization conditions.

The specification teaches the cDNA sequence of the SCA2 nucleic acid, namely SEQ ID NO: 1. The cDNA sequence is 4,367 nucleotides in length (SEQ ID NO: 1). The specification teaches that SEQ ID NO: 2 is the amino acid sequence which encodes the nucleic acid of SEQ ID NO: 1.

The claims are sufficiently broad to encompass full length genomic sequences, sequences from other species which would hybridize with SEQ ID NO: 1, and variants of the sequence which have not been described. The specification fails to describe the full length genomic sequences. Sahba et al. (Genomics, 47, pages 359-364, 1998) teaches the genomic structure of the SCA2 gene which has 25 exons, encompassing approximately 130kb. The instant specification does not provide any description for the full length gene, including introns, exon boundaries and regulatory regions.

Moreover, the claims encompass variants of SEQ ID NO: 1 which have not been described. The specification fails to describe any variants of SEQ ID NO: 1 aside from the single CAG repeat region between 166-188. The post filing date art provides examples of numerous polymorphisms which have not been described at the time the invention was made. For example, Choudhry et al (Human Mol. Genetics. Vol. 10, No. 21, pages 2437-2446, 2001) teaches two novel single nucleotide polymorphisms (SNPs) in exon 1. Moreover, Mizushima et al. (J. Med. Genet. Vol. 36, pages 112-114, 1999) teaches CCG or CCGCCG polymorphisms within expanded alleles. Neither of these examples were supported by the instant specification.

Furthermore, the claims encompass SCA2 nucleic acids from closely related species. For example, the partial sequence of the chimp, gorilla, rhesus monkey, leaf monkey, baboon and bonnet monkey, the approximately 300-400 base pair partial sequences are 99, 97, 95, 97, 96 and 94% homologous, respectively before the CAG repeat region and 100, 100, 100, 97, -, 100% homologous following the CAG repeat region (see NCBI blast results attached). These very closely related sequences have neither been described nor contemplated in the instant specification.

Unlike Example 9 of the Written Description Guidelines which is drawn to hybridization language, the claims are not drawn to an isolated cDNA that specifically hybridizes under specified conditions to the complement of SEQ ID NO: X, wherein said nucleic acid encodes a protein that has Y function. The instant claims do not contain any functional language. Moreover, the claims are not drawn to a full cDNA. Rather, the claims are drawn to nucleic acids comprising 2500 base pairs and 630 base pairs. Therefore, the claims fail to meet the description guidelines as compared to Example 9 of the Written Description Guidelines.

Therefore, the description in the specification as filed is not sufficient to convey that the applicant was, as of the filing date, in possession of the invention in a manner commensurate in scope with the claims. There is disclosed only a limited number of species, and applicants attempt to claim, on the basis of that single species, any nucleic acid comprising 2500 or 630 base pairs which hybridize under the specified conditions to SEQ ID NO: 1. Given this broad definition, the scope of the claims would appear to be much broader than the particularly disclosed species, and one is unable to envision,

and the specification does not adequately describe, a commensurate number of species. *Vas-Cath Inc. v. Mahurkar*, 19USPQ2d 1111, clearly states that “applicant must convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession of the *invention*. The invention is, for the purposes of the ‘written description’ inquiry, whatever is now claimed.” (See page 1117). The specification does not “clearly allow persons of ordinary skill in the art to recognize that [he or she] invented what is claimed.” (See *Vas-Cath* at page 1116). Therefore, only nucleic acids of SEQ ID NO: 1 or nucleic acids encoding SEQ ID NO: 2, but not the full breadth of the claims meets the written description provision of 35 U.S.C. §112, first paragraph.

Claim Rejections - 35 USC § 112- Second Paragraph

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

7. Claims 17 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

A) Claim 17 is indefinite because Claim 16 requires that the first oligonucleotide specifically hybridizes to SEQ ID NO: 1 between positions 4367 and 622. SEQ ID NO: 7 is a forward primer. Therefore, SEQ ID NO: 7 is located between positions 1-543. Hence it is unclear how SEQ ID NO: 7 may be the first oligonucleotide.

Conclusion

8. No claims allowable.


9. Any inquiry concerning this communication or earlier communications from the examiner should be directed to examiner Jeanine Goldberg whose telephone number is (703) 306-5817. The examiner can normally be reached Monday-Friday from 8:00 a.m. to 5:30 p.m.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Gary Jones, can be reached on (703) 308-1152. The fax number for this Group is (703) 305- 3014.

Any inquiry of formal matters can be directed to the patent analyst, Pauline Farrier, whose telephone number is (703) 305-3550.

Any inquiry of a general nature should be directed to the Group receptionist whose telephone number is (703) 308-0196.

Jeanine Goldberg
October 2, 2002


W. Gary Jones
Supervisory Patent Examiner
Technology Center 1600



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

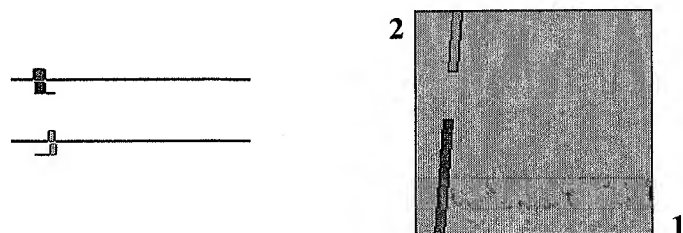
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.1 [Aug-1-2001]

 Match: Mismatch: gap open: gap extension:

 x_dropoff: expect: wordsize: Filter ☒ Align

Sequence 1 gi_4506794 Homo sapiens spinocerebellar ataxia 2 (olivopontocerebellar ataxia 2, autosomal dominant, ataxin 2) (SCA2), mRNA **Length** 4481 (1 .. 4481)
Sequence 2 gi_12382830 ^{Chimp} Pan troglodytes SCA2 gene, partial sequence. **Length** 390 (1 .. 390)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 379 bits (197), Expect = e-101
 Identities = 201/203 (99%)
 Strand = Plus / Plus

```

Query: 455 gcgggcctccccgcccccttcgtcgtcgtccttctccccctcgccagcccggcgccctc 514
          |||
Sbjct: 1   gcgggcctccccgcccccttcgtcgtcgtccttctccccctcgccagcccggcgccctc 60
  
```

```

Query: 515 cggccgcgccaaaccgcgcctccccgctcggcgcccggtgcgtccccgcgcgttccggcg 574
          |||
Sbjct: 61  cggccgcgccaaaccgcgcctccccgctcggcgcccgcggtccccgcgcgttccggcg 120
  
```

```

Query: 575 tctccttggcgcgcccggtccccggctgtccccgcccggcggtgcgagccggtgtatgggc 634
          |||
Sbjct: 121 tctccttggcgcgcccggtccccggctgtccccgcccggcggtgcgagccggtgtatgggc 180
  
```

```

Query: 635 ccctcaccatgtcgctgaagccc 657
          |||
Sbjct: 181 ccctcaccatgtcgctgaagccc 203
  
```

Score = 202 bits (105), Expect = 2e-48
 Identities = 105/105 (100%)
 Strand = Plus / Plus

Query: 725 cgccgcccgcggctgccaatgtccgcaagcccggcggcagcggccttctagcgtcgcccg 784
|||||
Sbjct: 286 cgccgcccgcggctgccaatgtccgcaagcccggcggcagcggccttctagcgtcgcccg 345

Query: 785 ccgcccgcgccttcgccgtcctcgtcctcggtctcctcgtcctcg 829
|||||
Sbjct: 346 ccgcccgcgccttcgccgtcctcgtcctcggtctcctcgtcctcg 390

CPU time: 0.08 user secs. 0.04 sys. secs 0.12 total secs.

Gapped

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2

Gap Penalties: Existence: 5, Extension: 2

Number of Hits to DB: 7

Number of Sequences: 0

Number of extensions: 7

Number of successful extensions: 6

Number of sequences better than 10.0: 1

length of query: 4481

length of database: 4,547,798,281

effective HSP length: 26

effective length of query: 4455

effective length of database: 4,546,331,309

effective search space: 20253905981595

effective search space used: 20253905981595

T: 0

A: 30

X1: 6 (11.5 bits)

X2: 26 (50.0 bits)

S1: 12 (23.8 bits)

S2: 21 (41.1 bits)



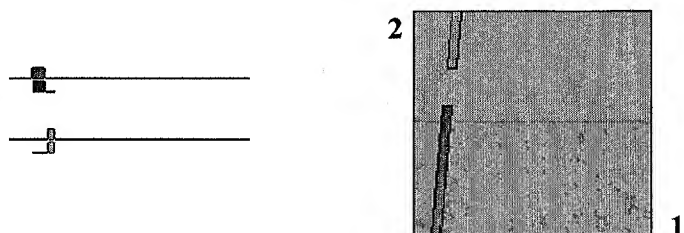
Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.1 [Aug-1-2001]

Match: Mismatch: gap open: gap extension:
 x_dropoff: expect: wordsize: ☐ Filter ☒ Align

Sequence 1 gi_4506794 Homo sapiens spinocerebellar ataxia 2 (olivopontocerebellar ataxia 2, autosomal dominant, ataxin 2) (SCA2), mRNA **Length** 4481 (1 .. 4481)
Sequence 2 gi_12382831 Gorilla gorilla SCA2 gene, partial sequence. **Length** 409 (1 .. 409)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 427 bits (222), Expect = e-116
 Identities = 232/237 (97%)
 Strand = Plus / Plus

```
Query: 421 tttcggccccggctcccgggcggtccttgggtctcggcgggcctccccgccccttcgtcgtc 480
      |||
Sbjct: 1   tttcggccccggctcccgggcggtccttgggtctcggcgggcctccccgccccttcgtcgtc 60
```

```
Query: 481 gtcctttctccccctcgccagcccgggcgcccctccggccgcgccaacccgcgcctccccg 540
      |||
Sbjct: 61  ctctttctccccctcgccagcccgggcgcccctccggccgtgccaacccgcgcctccccg 120
```

```
Query: 541 ctcggcgcccgtgctccccgcccgttccggcgtctccttggcgcgcccggctccccggc 600
      |||
Sbjct: 121 ctcagcgcccgcgctccccgcccgtccggcgtctccttggcgcgcccggctccccggc 180
```

```
Query: 601 tgtccccgcccggcggtgagccgggtgatgggcccctcaccatgtcgctgaagccc 657
      |||
Sbjct: 181 tgtccccgcccggcggtgagccgggtgatgggcccctcaccatgtcgctgaagccc 237
```

Score = 202 bits (105), Expect = 2e-48
 Identities = 105/105 (100%)
 Strand = Plus / Plus

Query: 725 cgccgccccgaggctgccaatgtccgcaagcccgaggcagcggccttctagcgtcgcccc 784
|||||
Sbjct: 305 cgccgccccgaggctgccaatgtccgcaagcccgaggcagcggccttctagcgtcgcccc 364

Query: 785 ccgccgcgccttcgccgtcctcgctcctcggtctcctcgtcctcgg 829
|||||
Sbjct: 365 ccgccgcgccttcgccgtcctcgctcctcggtctcctcgtcctcgg 409

CPU time: 0.08 user secs. 0.04 sys. secs 0.12 total secs.

Gapped

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2

Gap Penalties: Existence: 5, Extension: 2

Number of Hits to DB: 10

Number of Sequences: 0

Number of extensions: 10

Number of successful extensions: 7

Number of sequences better than 10.0: 1

length of query: 4481

length of database: 4,547,798,281

effective HSP length: 26

effective length of query: 4455

effective length of database: 4,546,331,309

effective search space: 20253905981595

effective search space used: 20253905981595

T: 0

A: 30

X1: 6 (11.5 bits)

X2: 26 (50.0 bits)

S1: 12 (23.8 bits)

S2: 21 (41.1 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

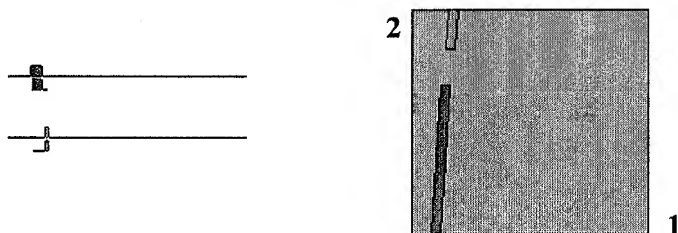
Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.1 [Aug-1-2001]

Match: Mismatch: gap open: gap extension:
 x_dropoff: expect: wordsize: ☒ Filter ☐ Align

Sequence 1 gi 4506794 Homo sapiens spinocerebellar ataxia 2 (olivopontocerebellar ataxia 2, autosomal dominant, ataxin 2) (SCA2), mRNA **Length** 4481 (1 .. 4481)
Sequence 2 gi 12382833 ^{rhesus monkey} Macaca mulatta SCA2 gene, partial sequence. **Length** 303 (1 .. 303)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 339 bits (176), Expect = 2e-89
 Identities = 194/203 (95%)
 Strand = Plus / Plus

Query: 455 gcgggcctccccgcccccttcgtcgtcgtccttctccccctcgccagcccgggcgccccctc 514
 Sbjct: 1 gcgggcctccccgcccccttcgtcgtcgtccttctcccccgccagcccgggtgcccccc 60

Query: 515 cggccgcgccaaccgcgcctccccgctcggcgcccggtgcgtccccgcgcggttcgggcg 574
 Sbjct: 61 cggccgcgccaaccgcgcctccctgctcggcgcccgcggtccccgcgcgctccgggcg 120

Query: 575 tctccttggcgcgcccggctccccggctgtccccgcccggcggtgcgagccggtgtatgggc 634
 Sbjct: 121 tctcctcggcgcgcccggctccccggctgtccccgcccggcggtgcgagccggtgtatgggc 180

Query: 635 ccctcaccatgtcgtgaagccc 657
 Sbjct: 181 ccctcaccatgtcgtgaagccc 203

Score = 102 bits (53), Expect = 3e-18
 Identities = 53/53 (100%)
 Strand = Plus / Plus

Query: 726 gccgccccgcggtgccaatgtccgcaagccccggcggcagcggccttctagcgt 778

Sbjct: 251 gccgccccgcggtgccaatgtccgcaagccccggcggcagcggccttctagcgt 303

CPU time: 0.10 user secs. 0.04 sys. secs 0.14 total secs.

Gapped

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2

Gap Penalties: Existence: 5, Extension: 2

Number of Hits to DB: 5

Number of Sequences: 0

Number of extensions: 5

Number of successful extensions: 5

Number of sequences better than 10.0: 1

length of query: 4481

length of database: 4,547,798,281

effective HSP length: 26

effective length of query: 4455

effective length of database: 4,546,331,309

effective search space: 20253905981595

effective search space used: 20253905981595

T: 0

A: 30

X1: 6 (11.5 bits)

X2: 26 (50.0 bits)

S1: 12 (23.8 bits)

S2: 21 (41.1 bits)



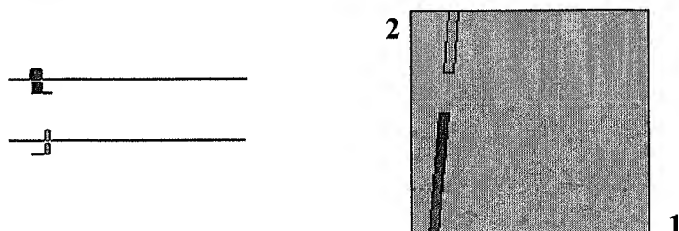
Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.1 [Aug-1-2001]

Match: Mismatch: gap open: gap extension:
 x_dropoff: expect: wordsize: Filter ☒ Align

Sequence 1 gi_4506794 Homo sapiens spinocerebellar ataxia 2 (olivopontocerebellar ataxia 2, autosomal dominant, ataxin 2) (SCA2), mRNA Length 4481 (1 .. 4481)
 Sequence 2 gi_12382832 ^{leaf mouth}Presbytis entellus SCA2 gene, partial sequence. Length 384 (1 .. 384)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 350 bits (182), Expect = 6e-93
 Identities = 200/209 (95%)
 Strand = Plus / Plus

```

Query: 449  gtctcggcgggcctccccgccccttcgtcgtcgtccttctccccctcgccagcccgggcg 508
           |||
Sbjct: 1    gtctcggcgggcctccccgccccttcgtcgtcgtccttctccccctcgccagcccgagt 60

Query: 509  cccctccggcgcgcgaaccgcgcctcccgctcggcgcccggtgcgtccccgcgcgtt 568
           |||
Sbjct: 61  ccccccggcgcgcgaaccgcgcctcccgctcagcgcccgcgctccccgcgcgct 120

Query: 569  ccggcgctctccttggcgcgcccggtcccggtgtccccgcccggcggtgcgagccggtgt 628
           |||
Sbjct: 121 ccggcgctctcctcggcgcgcccggtcccggtgtccccgcccggcggtgcgagccggtgt 180

Query: 629  atgggcccctcaccatgtcgtgaagccc 657
           |||
Sbjct: 181 atgggcccctcaccatgtcgtgaagccc 209
  
```

Score = 183 bits (95), Expect = 1e-42
 Identities = 101/104 (97%)
 Strand = Plus / Plus

Query: 726 gccgcccgcggctgccaatgtccgcaagccccggcggcagcggccttctagcgctcgcccgc 785
Sbjct: 281 gccgcccgcggctgccaatgtccgtaagccccggcggcagcggccttctagcgctcgcccgc 340

Query: 786 cgccgcgccttcgccgctcctcggtctcctcgtcctcgg 829
Sbjct: 341 cgccgcgccttcgccgctcctcggtctcctcgtcctcgg 384

CPU time: 0.09 user secs. 0.04 sys. secs 0.13 total secs.

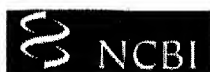
Gapped

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 6
Number of Sequences: 0
Number of extensions: 6
Number of successful extensions: 5
Number of sequences better than 10.0: 1
length of query: 4481
length of database: 4,547,798,281
effective HSP length: 26
effective length of query: 4455
effective length of database: 4,546,331,309
effective search space: 20253905981595
effective search space used: 20253905981595
T: 0
A: 30
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 21 (41.1 bits)



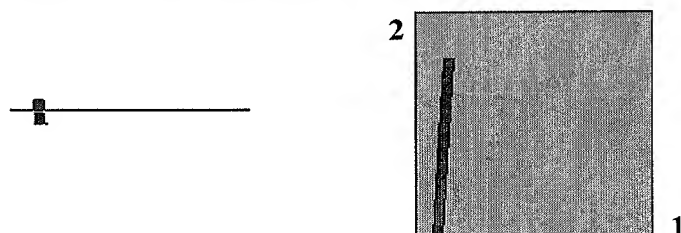
Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.1 [Aug-1-2001]

Match: Mismatch: gap open: gap extension:
 x_dropoff: expect: wordsize: Filter ☒ Align

Sequence 1 gi 4506794 Homo sapiens spinocerebellar ataxia 2 (olivopontocerebellar ataxia 2, autosomal dominant, ataxin 2) (SCA2), mRNA **Length** 4481 (1 .. 4481)
Sequence 2 gi 12382834 ^{baboon} Papio hamadryas SCA2 gene, partial sequence. **Length** 264 (1 .. 264)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 356 bits (185), Expect = 1e-94
 Identities = 201/209 (96%)
 Strand = Plus / Plus

```

Query: 449  gtctcggcgggcctccccgccccttcgtcgtcgtccttctccccctcgccagccccgggcg 508
           |||
Sbjct: 1    gtctcggcgggcctccccgccccttcgtcgtcctccttctccccctcggcagccccgggtc 60

Query: 509  cccctccggcgcgcgaaccgcgcctccccgctcggcgcccggtgcgtccccgcccgcgtt 568
           |||
Sbjct: 61  cccccccggcgcgcgaaccgcgcctccccgctcggcgcccgcgctccccgcccgcgt 120

Query: 569  cggcgctctccttggcgcgcccggtccccggctgtccccgcccggcgtgcgagccggtgt 628
           |||
Sbjct: 121 cggcgctctcctcggcgcgcccggtccccggctgtccccgcccggcgtgcgagccggtgt 180

Query: 629  atgggcccctcaccatgtcgctgaagccc 657
           |||
Sbjct: 181 atgggcccctcaccatgtcgctgaagccc 209
  
```

CPU time: 0.09 user secs. 0.04 sys. secs 0.13 total secs.

Gapped
 Lambda K H

1.33 0.621 1.12

Gapped

Lambda

K

H

1.33 0.621 1.12

Matrix: blastn matrix:1 -2

Gap Penalties: Existence: 5, Extension: 2

Number of Hits to DB: 5

Number of Sequences: 0

Number of extensions: 5

Number of successful extensions: 4

Number of sequences better than 10.0: 1

length of query: 4481

length of database: 4,547,798,281

effective HSP length: 26

effective length of query: 4455

effective length of database: 4,546,331,309

effective search space: 20253905981595

effective search space used: 20253905981595

T: 0

A: 30

X1: 6 (11.5 bits)

X2: 26 (50.0 bits)

S1: 12 (23.8 bits)

S2: 21 (41.1 bits)



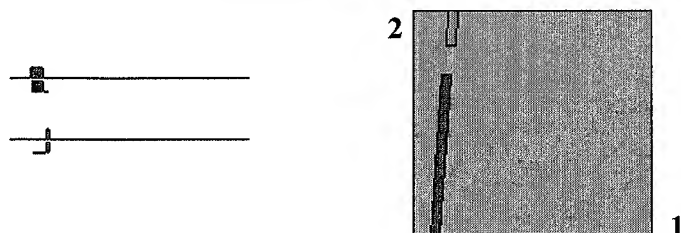
Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.1 [Aug-1-2001]

Match: Mismatch: gap open: gap extension:
 x_dropoff: expect: wordsize: Filter ☒ Align

Sequence 1 gi 4506794 Homo sapiens spinocerebellar ataxia 2 (olivopontocerebellar ataxia 2, autosomal dominant, ataxin 2) (SCA2), mRNA **Length** 4481 (1 .. 4481)
Sequence 2 gi 12382835 ^{monkey} Macaca radiata SCA2 gene, partial sequence. **Length** 322 (1 .. 322)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 377 bits (196), Expect = e-101
 Identities = 220/232 (94%)
 Strand = Plus / Plus

Query: 426 gcccggtcccgcggtccttggtctcggcggcctccccgccccttcgtcgctcgtcct 485
 Sbjct: 1 gcccggtcccgcgagctcctcggtctcggcggcctccccgccccttcgtcgctcctcct 60

Query: 486 tctccccctcgccagcccgggcgcccctccggccgcgccaaccgcgcctccccgctcgg 545
 Sbjct: 61 tctcccccgcgagcccgggcgcccccccgccgcgccaaccgcgcctccctgctcgg 120

Query: 546 cgcccggtcggtccccgcgcgttcggcggtctccttggcgcgcccggtcccggtgtcc 605
 Sbjct: 121 cgcccgcggtccccgcgcgttcggcggtctcctcggcgcgcccggtcccggtgtcc 180

Query: 606 ccgccccggcggtgcgagccgggtgtatgggcccctcaccatgtcgctgaagccc 657
 Sbjct: 181 ccgccccggcggtgcgagccgggtgtatgggcccctcaccatgtcgctgaagccc 232

Score = 94.9 bits (49), Expect = 5e-16
 Identities = 49/49 (100%)
 Strand = Plus / Plus

Query: 726 gccgccccgaggctgccaatgtccgcaagccccggcggcagcggccttcta 774
Sbjct: 274 gccgccccgaggctgccaatgtccgcaagccccggcggcagcggccttcta 322

CPU time: 0.12 user secs. 0.01 sys. secs 0.13 total secs.

Gapped

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2

Gap Penalties: Existence: 5, Extension: 2

Number of Hits to DB: 8

Number of Sequences: 0

Number of extensions: 8

Number of successful extensions: 6

Number of sequences better than 10.0: 1

length of query: 4481

length of database: 4,547,798,281

effective HSP length: 26

effective length of query: 4455

effective length of database: 4,546,331,309

effective search space: 20253905981595

effective search space used: 20253905981595

T: 0

A: 30

X1: 6 (11.5 bits)

X2: 26 (50.0 bits)

S1: 12 (23.8 bits)

S2: 21 (41.1 bits)